

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Ni, Jian
Yu, Guo-Liang
Gentz, Reiner
Rosen, Craig A.

(ii) TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STUART & OLSTEIN
(B) STREET: 6 Becker Farm Road
(C) CITY: Roseland
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07068

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/467,265
(B) FILING DATE: 06-JUN-1995
(C) CLASSIFICATION:

Sub A1
(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ferraro, Gregory D.
(B) REGISTRATION NUMBER: 36,134
(C) REFERENCE/DOCKET NUMBER: 325800-456

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 201-994-1700
(B) TELEFAX: 201-994-1744

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 31..843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAGGGAACGT	GTTTCTCCCC	TCGTTGGTC	ATG GAG GCG CTG CCC CTG CTA GCC	54
			Met Glu Ala Leu Pro Leu Leu Ala	
			1 5	
GCG ACA ACT	CCG GAC CAC	GGC CGC CAC	CGA AGG CTG CTT CTG CTG CCG	102
Ala Thr Thr	Pro Asp His	Gly Arg His	Arg Arg Leu Leu Leu Pro	
10	15	20		
CTA CTG CTG	TTC CTG CTG	CCG GCT GGA GCT	GTG CAG GGC TGG GAG ACA	150
Leu Leu Leu	Phe Leu Leu	Pro Ala Gly	Val Gln Gly Trp Glu Thr	
25	30	35	40	
GAG GAG AGG CCC CGG	ACT CGC GAA GAG GAG	TGC CAC TTC TAC GCG GGT		198
Glu Glu Arg Pro	Arg Thr Arg Glu	Glu Glu Cys His Phe Tyr Ala Gly		
45	50	55		
GGA CAA GTG TAC	CCG GGA GAG GCA TCC CCG GTA TCG GTC	GCC GAC CAC		246
Gly Gln Val	Tyr Pro Gly Glu Ala Ser	Arg Val Ser Val Ala Asp His		
60	65	70		
TCC CTG CAC CTA ACC	AAA GCG AAG ATT TCC AAG CCA GCG CCC	TAC TGG		294
Ser Leu His Leu Ser	Lys Ala Lys Ile Ser Lys Pro	Ala Pro Tyr Trp		
75	80	85		
GAA GGA ACA GCT GTG	ATC GAT GGA GAA TTT AAG GAG CTG AAG TTA ACT			342
Glu Gly Thr Ala Val	Ile Asp Gly Glu Phe Lys Glu Leu Lys Leu Thr			
90	95	100		
GAT TAT CGT GGG AAA	TAC TTG GTT TTC TTC	TAC CCA CTT GAT TTC		390
Asp Tyr Arg Gly Lys	Tyr Leu Val Phe Phe	Phe Tyr Pro Leu Asp Phe		
105	110	115	120	
ACA TTT GTG TGT CCA ACT	GAA ATT ATC GCT TTT GGC GAC AGA CTT GAA			438
Thr Phe Val Cys Pro	Thr Glu Ile Ile Ala Phe Gly Asp Arg	Leu Glu		
125	130	135		
GAA TTC AGA TCT ATA AAT ACT GAA GTG GTA GCA TGC TCT GTT GAT TCA				486
Glu Phe Arg Ser Ile Asn Thr	Glu Val Val Ala Cys Ser Val Asp Ser			
140	145	150		
CAG TTT ACC CAT TTG GCC TGG	ATT AAT ACC CCT CGA AGA CAA GGA GGA			534
Gln Phe Thr His Leu Ala Trp	Ile Asn Thr Pro Arg Arg Gln Gly Gly			
155	160	165		
CTT GGG CCA ATA AGG ATT CCA	CTT CTT TCA GAT TTG ACC CAT CAG ATC			582
Leu Gly Pro Ile Arg Ile Pro	Leu Leu Ser Asp Leu Thr His Gln Ile			
170	175	180		
TCA AAG GAC TAT GGT GTA TAC CTA GAG GAC TCA GGC CAC ACT CTT AGA				630
Ser Lys Asp Tyr Gly Val Tyr Leu Glu Asp Ser Gly His Thr Leu Arg				
185	190	195	200	
GGT CTC TTC ATT ATT GAT GAC AAA GGA ATC CTA AGA CAA ATT ACT CTG				678
Gly Leu Phe Ile Ile Asp Asp Lys Gly	Ile Leu Arg Gln Ile Thr Leu			
205	210	215		

AAT GAT CTT CCT GTG GGT AGA TCA GTG GAT GAG ACA CTA CGT TTG GTT	726
Asn Asp Leu Pro Val Gly Arg Ser Val Asp Glu Thr Leu Arg Leu Val	
220 225 230	
CAA GCA TTC CAG TAC ACT GAC AAA CAC GGA GAA GTC TGC CCT GCT GGC	774
Gln Ala Phe Gln Tyr Thr Asp Lys His Gly Glu Val Cys Pro Ala Gly	
235 240 245	
TGG AAA CCT GGT AGT GAA ACA ATA ATC CCA GAT CCA GCT GGA AAG CTG	822
Trp Lys Pro Gly Ser Glu Thr Ile Ile Pro Asp Pro Ala Gly Lys Leu	
250 255 260	
AAG TAT TTC GAT AAA CTG AAT TGAGAAATAC TTCTTCAAGT TATGATGCTT	873
Lys Tyr Phe Asp Lys Leu Asn	
265 270	
GAAAAGTTCTC AATAAAGTTTC ACGGTTTCAT TACCACAAAAA AAAAAA	
	918

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Ala Leu Pro Leu Leu Ala Ala Thr Thr Pro Asp His Gly Arg	
1 5 10 15	
His Arg Arg Leu Leu Leu Leu Pro Leu Leu Leu Phe Leu Leu Pro Ala	
20 25 30	
Gly Ala Val Gln Gly Trp Glu Thr Glu Glu Arg Pro Arg Thr Arg Glu	
35 40 45	
Glu Glu Cys His Phe Tyr Ala Gly Gly Gln Val Tyr Pro Gly Glu Ala	
50 55 60	
Ser Arg Val Ser Val Ala Asp His Ser Leu His Leu Ser Lys Ala Lys	
65 70 75 80	
Ile Ser Lys Pro Ala Pro Tyr Trp Glu Gly Thr Ala Val Ile Asp Gly	
85 90 95	
Glu Phe Lys Glu Leu Lys Leu Thr Asp Tyr Arg Gly Lys Tyr Leu Val	
100 105 110	
Phe Phe Phe Tyr Pro Leu Asp Phe Thr Phe Val Cys Pro Thr Glu Ile	
115 120 125	
Ile Ala Phe Gly Asp Arg Leu Glu Glu Phe Arg Ser Ile Asn Thr Glu	
130 135 140	
Val Val Ala Cys Ser Val Asp Ser Gln Phe Thr His Leu Ala Trp Ile	
145 150 155 160	

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Asn Thr Pro Arg Arg Gln Gly Gly Leu Gly Pro Ile Arg Ile Pro Leu
165 170 175

Leu Ser Asp Leu Thr His Gln Ile Ser Lys Asp Tyr Gly Val Tyr Leu
180 185 190

Glu Asp Ser Gly His Thr Leu Arg Gly Leu Phe Ile Ile Asp Asp Lys
195 200 205

Gly Ile Leu Arg Gln Ile Thr Leu Asn Asp Leu Pro Val Gly Arg Ser
210 215 220

Val Asp Glu Thr Leu Arg Leu Val Gln Ala Phe Gln Tyr Thr Asp Lys
225 230 235 240

His Gly Glu Val Cys Pro Ala Gly Trp Lys Pro Gly Ser Glu Thr Ile
245 250 255

Ile Pro Asp Pro Ala Gly Lys Leu Lys Tyr Phe Asp Lys Leu Asn
260 265 270

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
- (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCAGCGGATCC ATGGAGGCGC TGCCCTGCT

29

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
- (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGCCCCATGGA GGCCTGCC CTG

23

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGCCCATGGC TGGAGCTGTG CAGGG

25

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGCGTCTAGA TCAATTCACT TTATCGAAAT ACTTCAGC

38

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGCGGATCC GCTGGAGCTG TGCAGG

26

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGCGGATCCC GAGGCCTGC CCCTGC

26

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGCGGATCCT CAATTCAAGTT TATCGAAATA C

31

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGCGGATCCG CCATCATGGA GGCGCTGCCCTG

33

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

Sequence Database

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGCGGATCCT CAATTCAAGTT TATCGAAATC A

31

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCGCGGATCC ACCATGGAGG CGCTG

25

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCGCTCTAGA TCAAGCGTAG TCTGGGACGT CGTATGGGTA ATTCAAGTTA TC

52

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(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Ser Ser Gly Asn Ala Lys Ile Gly His Pro Ala Pro Asn Phe Lys

1 5 10 15

Ala Thr Ala Val Met Pro Asp Gly Gln Phe Lys Asp Ile Ser Leu Ser
 20 25 30

Asp Tyr Lys Gly Lys Tyr Val Val Phe Phe Tyr Pro Leu Asp Phe
 35 40 45

Thr Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asp Arg Ala Glu
 50 55 60

Glu Phe Lys Lys Leu Asn Cys Gln Val Ile Gly Ala Ser Val Asp Ser
 65 70 75 80

His Phe Cys His Leu Ala Trp Val Asn Thr Pro Lys Lys Gln Gly Gly
 85 90 95

Leu Gly Pro Met Asn Ile Pro Leu Val Ser Asp Pro Lys Arg Thr Ile
 100 105 110

Ala Gln Asp Tyr Gly Val Leu Lys Ala Asp Glu Gly Ile Ser Phe Arg
 115 120 125

Gly Leu Phe Ile Ile Asp Asp Lys Gly Ile Leu Arg Gln Ile Thr Val
 130 135 140

Asn Asp Pro Pro Cys Cys Arg Ser Val Asp Glu Thr Leu Arg Leu Val
 145 150 155 160

Gln Ala Phe Gln Phe Thr Asp Lys His Gly Glu Val Cys Pro Ala Gly
 165 170 175

Trp Lys Pro Gly Ser Asp Thr Ile Lys Pro Asp Val Pro Lys Thr Lys
 180 185 190

Glu Tyr Phe Ser Lys Gln Lys
 195

(2) INFORMATION FOR SEQ ID NO:15:

- bulk A1
GDP*
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Ala Ser Gly Asn Ala Arg Ile Gly Lys Pro Ala Pro Asp Phe Lys
 1 5 10 15

Ala Thr Ala Val Val Asp Gly Ala Phe Lys Glu Val Lys Leu Ser Asp
 20 25 30

Tyr Lys Gly Lys Tyr Val Val Leu Phe Phe Tyr Pro Leu Asp Phe Thr
 35 40 45

Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asn Arg Ala Glu Asp
 50 55 60

Phe Arg Lys Leu Gly Cys Glu Val Leu Gly Val Ser Val Asp Ser Gln
 65 70 75 80

Phe Asn His Leu Ala Trp Ile Asn Thr Pro Arg Lys Glu Gly Leu
 85 90 95

Gly Pro Leu Asn Ile Pro Leu Leu Gly Asp Val Thr Arg Arg Leu Ser
 100 105 110

Glu Asp Tyr Gly Val Leu Lys Thr Asp Glu Gly Ile Ala Tyr Arg Gly
 115 120 125

Leu Phe Ile Ile Asp Gly Lys Gly Val Leu Arg Gln Ile Thr Val Asn
 130 135 140

Asp Leu Pro Val Gly Arg Ser Val Asp Glu Ala Leu Arg Leu Val Gln
 145 150 155 160

Ala Phe Gln Tyr Thr Asp Glu His Gly Glu Val Cys Pro Ala Gly Trp
 165 170 175

Lys Pro Gly Ser Asp Thr Ile Lys Pro Asn Val Asp Asp Ser Lys Glu
 180 185 190

Tyr Phe Ser Lys His Asn
 195

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 257 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Ala Ala Ala Ala Gly Arg Leu Leu Trp Ser Ser Val Ala Arg Gly
 1 5 10 15

Ala Ser Ala Ile Ser Arg Ser Ile Ser Ala Ser Thr Val Leu Arg Pro
 20 25 30

Val Ala Ser Arg Arg Thr Cys Leu Thr Asp Ile Leu Trp Ser Ala Ser
 35 40 45

Ala Gln Gly Lys Ser Ala Phe Ser Thr Ser Ser Ser Phe His Thr Pro
 50 55 60

100-200-300-400-500

Ala Val Thr Gln His Ala Pro Tyr Phe Lys Gly Thr Ala Val Val Asn
65 70 75 80

Gly Glu Phe Lys Glu Leu Ser Leu Asp Asp Phe Lys Gly Lys Tyr Leu
85 90 95

Val Leu Phe Phe Tyr Pro Leu Asp Phe Thr Phe Val Cys Pro Thr Glu
100 105 110

Ile Val Ala Phe Ser Asp Lys Ala Asn Glu Phe His Asp Val Asn Cys
115 120 125

Glu Val Val Ala Val Ser Val Asp Ser His Phe Ser His Leu Ala Trp
130 135 140

Ile Asn Thr Pro Arg Lys Asn Gly Gly Leu Gly His Met Asn Ile Thr
145 150 155 160

Leu Leu Ser Asp Ile Thr Lys Gln Ile Ser Arg Asp Tyr Gly Val Leu
165 170 175

Leu Glu Ser Ala Gly Ile Ala Leu Arg Gly Leu Phe Ile Ile Asp Pro
180 185 190

Asn Gly Val Val Lys His Leu Ser Val Asn Asp Leu Pro Val Gly Arg
195 200 205

Ser Val Glu Glu Thr Leu Arg Leu Val Lys Ala Phe Gln Phe Val Glu
210 215 220

Thr His Gly Glu Val Cys Pro Ala Asn Trp Thr Pro Glu Ser Pro Thr
225 230 235 240

Ile Lys Pro Ser Pro Thr Ala Ser Lys Glu Tyr Phe Glu Lys Val His
245 250 255

Gln

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(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 199 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Ser Ser Gly Asn Ala Lys Ile Gly Tyr Pro Ala Pro Asn Phe Lys
1 5 10 15

Ala Thr Ala Val Met Pro Asp Gly Gln Phe Lys Asp Ile Ser Leu Ser

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20 25 30

Glu Tyr Lys Gly Lys Tyr Val Val Phe Phe Phe Tyr Pro Leu Asp Phe
35 40 45

Thr Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asp Arg Ala Asp
50 55 60

Glu Phe Lys Lys Leu Asn Cys Gln Val Ile Gly Ala Ser Val Asp Ser
65 70 75 80

His Phe Cys His Ile Ala Trp Ile Asn Thr Pro Lys Lys Gln Gly Gly
85 90 95

Leu Gly Pro Met Asn Ile Pro Leu Ile Ser Asp Pro Lys Arg Thr Ile
100 105 110

Ala Gln Asp Tyr Gly Val Leu Lys Ala Asp Glu Gly Ile Ser Phe Arg
115 120 125

Gly Leu Phe Ile Ile Asp Asp Lys Gly Ile Leu Arg Gln Ile Thr Ile
130 135 140

Asn Asp Leu Pro Val Gly Arg Ser Val Asp Glu Ile Ile Arg Leu Val
145 150 155 160

Gln Ala Phe Gln Phe Thr Asp Lys His Gly Glu Val Cys Pro Ala Gly
165 170 175

Trp Lys Pro Gly Ser Asp Thr Ile Lys Pro Asp Val Asn Lys Ser Lys
180 185 190

Glu Tyr Phe Ser Lys Gln Lys
195